U.S. DEPARTMENT OF COMMERCE Patent and Trademark Office

#### **SEARCH REQUEST FORM**

Requestor's Name:		Serial Number:		_
Date:	Phone:	· · · · · · · · · · · · · · · · · · ·	Art Unit:	_
Search Topic: Please write a detailed statement of terms that may have a special meaniplease attach a copy of the sequence	ing. Give examples or relev	vent citations, authors, keyv	ject matter to be searched. Define any vords, etc., if known. For sequences, relevent claim(s).	· · · ·
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	STAFF	USE ONLY		
Date completed: 07-24- Searcher: Rejerty Co Terminal time: 20		earch Site STIC CM-1	VendorsIGSTN	· Paragonophija
Elapsed time:	T	Pre-S  ype of Search	Dialog APS	
Total time: 25  Number of Searches:		N.A. Sequence A.A. Sequence	Geninfo SDC	
Number of Databases:		Structure  Bibliographic	DARC/Questel Other (G,)	

PTO-1590 (9-90)

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### ALIGNMENTS

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	source	FEATURES	•								COMMENT	CONTENT	JOURNAL		TITLE		AUTHORS	REFERENCE		ORGANISM	SOURCE	VERSION	ACCESSION	DEFINITION	Locus	RESULT 1 AW619529/c
/organism="Sus Scrota" /db_xref="taxon:9823" /clone_lib="MARC PBE" /tlssue_type="Day 12 whole embryos" /lab_host="XLOLR" 12 whole embryos" /lab_host="XLOLR" 12 whole embryos in spherical and XhoI; Library made from pool of embryos in spherical and	L	Location/Qualifiers	BACKWARD: GTAAAACGACGGCCAGT Seq primer: AATTAACCCTCACTAAAGGG.	FORWARD: GGAAACAGCTATGACCATG	and -minmatch 12 options.	v0.980904.e. Vector identified by cross_match with the -minscore 18	Email: smith@email.marc.usda.gov	Fax: 402 762 4390	Tel: 402 762 4366	PO Box 166, Clay Center, NE 68933-0166, USA	TODA ANG TO Mest Arimal Persearch Center	3)3+1)4+1	Anim. Genet. 32 (2), 66-72 (2001)	cDNA library	Mapping of expressed sequence tags from a porcine early embryonic	,C.E. and Keele,J.W.	Smith, T.P.L., Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad	Mammalla; Eutherla; Cetartlodactyla; Sulna; Suldae; Sus. 1 (bases 1 to 332)	; Metazoa; Chordata; Craniata; Vertebrata;	Sus scrofa	D1a.	AW619529.1 GI:7325713		C PBE Sus scrofa cDNA 5', mRNA sequence.	AW619529 332 bp mRNA linear EST 24-MAR-2000	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AV398499 Bombyx mori ovary BmNPV infected; 2 hr after inoculation Bombyx mori cDNA clone NV021882 T3, mRNA sequence.

AV398499 GI:6902151
                                                                                                                                                                                                                                                                        Genome Research Group
Genome Research Group
National Institute of Radiological Sciences
Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 731)

Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA
Dombyx mori cDNA
Dombyshished (2000)
                                                                                                                                                                                             Project='Silkworm Genome Program in MAFF, and Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    domestic silkworm.
                                                                                                                                                                                                                                                                 method:uni-directional, sequence direction:sequenced from T3 primer
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68 c 74 g 96 t
               /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr
171 c 164 q 202 +
                                                                                                              /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV021882"
                                                                                                                                                                                Location/Qualifiers
                                                                                 inoculation"
                                                                                                /clone_lib="Bombyx mori ovary BmNPV
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92.7%;
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97104 MARC :
AW659631
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
Mammalia; E
                                                                                                                                                                                                                                                                                                                                                              Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                     BACKWARD: GTTTTCCCAGTCACGACG
Plate: 68 row: N column: 3
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                          Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscorv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA libraries and construction of a gene index for cattle Genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 240)
Smith, T.P.L., Grosse, W.M.,
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                                                                                                                                                                                                                                                             FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                             PCR PRimers
                                                                                                                                                                                                                                                                                             and -minmatch 12 options.
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                 70
              /note-"Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fit, hypothalamus, and pituitary."

51 c 52 g 67 t
                                                                                                                    /db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                                                                                                                     Location/Qualifiers
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                                                                                  /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                       organism-"Bos taurus"
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1BOV Bos taurus cDNA
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Pred. No. 4.
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Query Match Best Local Similarity

45.4%;

Score 140.4; DB 9; Pred. No. 3.2e-28;

Length 240

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RESULT 4
AI547008/c
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              75
                                                                                                                                                                                                   9 taataagatgaaaaaaatgttattttctgccgctctggcaatgcttattacaggatgtgc 68
                                                                                                                                   --tcaacaaacgtttactgttggaaac-aaaccgacagtagtaacaccaaaggaaacc-a 124
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                                                              TAATACGACTCNCTATANGGCNAATTTGGTACCGGNCCCCCTGCCTANTACAGGAAGNTC 196
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                           | tttgtggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaatggat 244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGTTGTTAAAACAGAAACCCACCAAACATTCGTAAATGGATTGCTCGGTTTTATTACTT
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              TTTGTGGCGGCGCAGAAAATGTTGTTAAAAACAGAAACCCCAGCAAACATTCGTAANANGAT 16
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PN2.1_13_C01.r mynorm Homo
AI547008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  University of Washington
Department of Molecular Biotechnology,
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l (bases 1 to 785)
Huang,G.M., Ng,W.l., Farkas,J., He,L., Liang,H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate cancer expression profiling by Genomics 59 (2), 178-186 (1999)
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                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       huanggm@yahoo.com
                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone_lib="mynorm"
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit cDNA library was constructed from a frozen normal (Stratagene). mRNA was extracted from a frozen normal prostate tissue (Mayo Clinic)."
a 128 c 147 g 229 t 128 others
                                                                                                                                                                                                                                                                                                                                                                                                                                       ocation/Qualifiers
                                                                                                                                                                                                                                           45.2%;
78.0%;
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tgctcaacaaacgtttactgttggaaacaaaccgacagcagtaacaccaaaaggaaaccat 125
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Citrus unshiu.
Citrus unshiu
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.
160
BG895793
359430 MARC 1PIG Sus scrofa
BG895793
BG895793.1 GI:14306034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Citriculture
National Institute of Fruit Tree Science,
Okitsu, Shimizu, Shizuoka 424-02, Japan
Tel: +81-543-69-2111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hisada,S., Akihama,T., Endo,T., Moriguchi,T. and Omura,M. Expressed sequence tags of Citrus fruit during rapid cell development phase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Mitsuo Omura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 223)
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r = Citrus Genome Analysis
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/dev_stage="rapid developing stage"
50 c 52 g 51 t
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/strain-"Miyaswa-wase satsuma
/db_xref-"taxon.55188"
/clone-"pcMFRI719.66"
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                                                                                                                                                                                                                                                                                                                                                 gctcacaata 308
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353618 MARC 1PIG Sus scrofa c
BG835172
BG835172.1 GI:14201080
EST.
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.

1 (bases 1 to 160)

Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.P.L., Casas, E., Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W.
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Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCAGGACG
Plate: 123 row: L column: 23
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
single pass sequencing. Bases called and alt_trimmed wi
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Sus scrofa
                                                                                                                                 Sus scrofa
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Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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Box 166, Clay Center, NE 68933-0166, USA
                                Keele, J.W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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/db_xref="taxon:9823"
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93.88;
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Pred. No. 7.1e-22;
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                                                                                                                                                                                                              mRNA sequence
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                                                                                              Euteleostomi;
Sus.
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Laegreid,W.W.
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Sus.
                                                                                                                                                                                                                                 EST 25-MAY-2001
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JOURNAL
COMMENT
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AUTHORS
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MEDLINE
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                                                                                                                        l (bases 1 to 336)

1 (bases 1 to 336)

1 (bases 1 to 336)

White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de William, O., Jaworski,J.G., Ohlrogge,J. and Benning,C.

A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil plant physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                  BE521841 336 bp M22A1STM Arabidopsis developing clone M22A1 5', mRNA sequence.
                                                                                                                                                                                                                                              Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core budicots;
Rossidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                           Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BACKWARD: GTTTTCCCAGTCACGACG
Plate: 116 row: L column: 23
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Smith TPL
Tel: 517 355 1609
Fax: 517 353 9334
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Fax: 402 762 4390
                                                   224 Biochemistry, Michigan State University,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
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/clone_lib="MARC 1PIG"
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                                                                                                                                                                                                                                                                                                                                                                     GI:9779819
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93.1%;
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Pred. No. 1.9e-21;
0; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                     seed Arabidopsis thaliana cDNA
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Email: benning@msu.edu

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JOURNAL COMMENT
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Best Local :
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                                                                                                                                      Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with
v0.980904.e. Vector identified by cross_match with the -mi
and -minmatch 12 options.
                                                                                                                                                                                                            USDA, ARS, US Meat Animal
PO Box 166, Clay Center, N
Tel: 402 762 4366
Fax: 402 762 4390
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                                                                                                                                                                                                                                                                                                                                                      Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sus scrofa
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363710 MARC 1PIG Sus scrofa cDNA
                                                                                  FORWARD: AGGAAACAGCTATGACCAT
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                                                                                                                                                                                                                                                                                                                                     Design and use of two pooled tissue normalized cDNA libraries for
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                                               Plate: 132 row: L column: 23
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                         PCR PRimers
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Site_1: EcoRI; Site_2: XhoII"
80 c 74 g 73 t
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/t1ssue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col1"
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/strain="Columbia"
/db_xref="taxon:3702"
/organism="Sus scrofa"
                               Location/Qualifiers
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NE 68933-0166, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytophthora infestans, Compatible Interaction
Unpublished (2000)
Contact: Octor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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EST535576 P. infestans-challenged leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Cathy Ronning
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/cline_lib="P. infestans-challenged leaf".
/tlssue_type="leaf"
/tlssue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
/lab_host="SOLR"
/lab_host="SOLR"
/note="Vector: pBluescript SK(-); Site_1: EcoRI; Site_2:
/note="Vector: pBluescript SK(-); Site_1: EcoRI; 
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/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
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/clone="PPCAW11"
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AI546999
                                                                                                                                                                                                                                                                                                                                                                       University of Washington
Department of Molecular Biotechnology, Box 357730, University of
Washington, Seattle, WA 98195
Tel: 5106280100
Fax: 5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Prostate cancer expression profiling by Genomics 59 (2), 178-186 (1999) 99339982
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 802)
Hugng,G.M., Ng,W.l., Farkas,J., He,L., Liang,H.A., Gordon,D., Yu,J.
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                                                                                                                                                                                                                                                                                                                                             huanggm@yahoo.com.
Location/Qualifiers
                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/db_meinb="mynorm"
/clone_lib="mynorm"
/note="Organ: Prostate; Vector: pBluescript; Directional cDNA library was constructed using Lambda ZP II kit cDNA library was constructed from a frozen normal (Stratagene). mRNA was extracted from a frozen normal prostate tissue (Mayo Clinic)."
a 152 c 163 g 183 t 125 others
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Pred. No. 5.8e-14;
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Pred. No. 1.2e-07;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                 64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
884811 560 bp DNA linear RPCI11-28F7.TP RPCI-11 Homo sapiens genomic clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsila, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C. The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae;
Triticeae; Secale.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Secale cereale
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomes - Anther cDNA library from rye
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      greenhouse. Anthers were harvested and pooled from early melosis to late meiosis. The tissue, total RNA, and poly(A) RNA were prepared (Butler, Ross and Gustafson) at University of Missouri, Columbia. A CDNA library was made, and the CDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Adult plant before anthesis"
/lab_host="E. col1 SOLR"
/note="Vector: Lambda Unl-LAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in t
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/clone="WHE1276_B06_C12"
/clone_lib="Secale cereale anther cDNA library"
/tissue_type="Anther"
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Pred. No. 4.
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Mismatches 7
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RPCI-11-28F7, DNA
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                                                                                                                                                                                                                                                                     TATCTCTCATCATGGATTATAAAATTCTATACTAGAGAACCCTGGAGACACCACCAAAGA 448
                                                                                                                                                                                                                                                                                                                                         ATTAGAACAAGACAAGGATGCTTACTTTTGCTACTCCCATCCAACATAGTACTAGAAGTG 328
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GSS.
   AQ309897 634 bp CITBI-E1-2522C23.TR CITBI-E1 Homo DNA sequence.
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Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or f
Research Genetics (info@resgen.com). BAC end search page:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, Tel: 301 838 0200 Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1998)
Other_GSSs: RPCI11-28F7.TV
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Use of BAC End Sequences for Sequence-Ready Map Building (1998)
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Seq primer: SP6
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/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
RPCII1 Human Male BAC Library"
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/clone="RPCI-11-28F7"
/clone_11b="RPCI-11"
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/db_xref="GDB:7510494"
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Pred. No. 0.049;
0; Mismatches 128;
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                    sapiens
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AQ544521.1 G
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                                                 AQ544521 532
CITBI-E1-2636G14.TR CITBI-E1
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http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
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Other_GSSs: CITBI-E1-2522C23.TF
Other_GSSs: CITBI-E1-2522C23.TF
Contact: Shaying Zhao, William Nierman,
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 301 838 0200
Fax: 301 838 0208
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Berry;K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Similarity 48.8%;
22; Conservative
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/note="Vector: pBeloBAC11; Site_1:
CalTech Human BAC Library D"
123 c 89 g 148 t
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/db_xref="taxon:9606"
/clone="2522C23"
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Pred. No. 0.05;
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AUTHORS
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SOURCE .
ORGANISM
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ORIGIN
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Search completed: July 23, 2002, 13:10:31 Job time: 7537 sec
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 13.9
Best Local Similarity 50.5
Matches 104; Conservative
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                                                                                                  430 TATCTCTCATCATGGATTATAAAATTCTATACTAGAGAACCCTGGAGACACCACCAAAGA 489
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                                                                                                                                                                                                                                                                                                  68 ctcaacaaacgtttactgttggaaacaaaccgacagcagtaacaccaaaggaaaccatca 127
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter,J.C.
Use of BAC End Sequences from CalTech Libraries for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and
Venter,J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ontact: Shaying Zhao, William Nierman, Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ones are available from Research Genetics (info@resgen.com). BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ublished (1997)
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301 838 0208
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/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
102 c 80 g 125 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'organism="Homo sapiens"
'db_xref="taxon:9606"
'clone="2636G14"
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                                                                                                                                                                                                                                                                                                                                                                                                                                              13.98;
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Title: Perfect score: Sequence:

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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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US-09-282-352A-5
US-09-023-221A-5
US-09-023-221A-6
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TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41.287
REFERENCE/DOCKET NUMBER: 255.00010101
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (612) 305-12
TELEFAX: (612) 305-122
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCODING
NUMBER OF SEQUENCES: 22
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                                                                                                                                          Local Similarity
mes 309; Conserv
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                                                           1 atgcaggataataagatgaaaaaaatgttattttctgccgctctggccaatgcttattaca
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B: MUETING, RAASCH & GEBHARDT P.A.

119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                       100.0%; ilarity 100.0%; Conservative 0
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US-08-718-892-1

US-08-714-918-84

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US-09-265-315-84

US-09-265-315-84

US-09-265-315-84

US-09-265-315-84

US-09-265-417-84

US-09-265-417-81

US-08-904-263A-3

US-08-904-263A-3

US-08-913-6378-189

US-08-918-638-15

US-08-918-614-1

US-09-385-982-25

US-08-691-871-5

US-08-698-614-3
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Pred. No. 5.4e-86;
Pred. No. 5.4e-86;
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                                                                                                                                                                                                            TELEFAX: (612) 305-122 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0:
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
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                                             Local Similarity
hes 309; Conserv
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                                                                                                                                                              LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                    NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/0 FILING DATE: 31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                          Score 309; DB 4;
Pred. No. 5.4e-86;
Mismatches 0;
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; TOPOLOGY: 1:
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US-09-023-221A-21
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Matches 309;
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                                                                                                                                                                                                                                                                                    TELEFAX: (612) 305-12 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
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ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
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APPLICANT: HORNE, SHELLEY M.
TITLE OF INVENTION: DNA ENCO
NUMBER OF SEQUENCES: 22
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34 ATGCAGGATAATAAGATGAAAAAATGTTATTTTCTGCCGCTCTGGCAATGCTTATTACA 93
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REFERENCE/DOCKET NUMBER: 255.00
                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-FEB-1998
CLASSIFICATION: 435
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STATE: MN
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                  1 atgcaggataataagatgaaaaaaatgttattttctgccgctctggccaatgcttattaca
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                                                                     Score 309; DB 3;
Pred. No. 5.8e-86;
; Mismatches 0;
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Best Local Similarity
Matches 309; Conserv
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                                                                                                                                                                                               TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                            TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (612) 305-1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS NUMBER OF SEQUENCES: 22
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                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                     LENGTH:
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1 atgcaggataataagatgaaaaaaatgttattttctgccgctctggccaatgcttattaca 60
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HORNE, SHELLEY M.
ROBINSON, MICHAEL
                                           Conservative
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                                                        100.0%;
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                                      Score 309; DB 4;
Pred. No. 5.8e-86;
Pred. No. 5.8e-86;
                                                                    Length 378;
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                                                                                                  US-09-023-221A-1
Query Match
Best Local Similarity
Matches 309; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/09023221A Patent No. 6087128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION: APPLICANT: NOLAN,
                                                                                                                                                                                                                                    TELEFAX: (612) 305-1228
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 25
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Release #1.0, VICURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:

"ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 760 base pairs
                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 tcacaatag 309
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                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                          NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 12-FE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34 ATGCAGGATAATAAGATGAAAAAAATGTTATTTCTGCCGCTCTGGCAATGCTTATTACA 93
                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GATTGCTCGGTTTTATCACTTTTGGCATCTATACTCCGCTGGAAGCCCGGGTATATTGC
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                                                                                                                                                                        nucleic acid
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HORNE, SHELLEY M.
VENTION: DNA ENCODING AN AVIAN
EQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
                                                                                                                                        linear
                                                                                                                                                                                                                                                                                                                                                                                                            12-FEB-1998
                                                                                                                  DNA (genomic)
                                                                                                                                                          single
                  100.0%;
                                                                                                                                                                                                                                                                                                                  255.00010101
Score 309; DB 3;
Pred. No. 7.6e-86;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Version #1.30
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                                      Length 760;
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ATGCAGGATAATAAGATGAAAAAAATGTTATTTTCTGCCGCTCTGGCAATGCTTATTACA 351 atgcaggataataagatgaaaaaaatgttattttctgccgctctggcaatgcttattaca

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US-09-282-352A-1
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                                            Matches
                                                            Query Match
Best Local :
                                                                                                                                                                                                                                      PRIOK AFFICATION NUMBER: US 09/UZ3,221
APPLICATION NUMBER: US 09/UZ3,221
FILING DATE: 12-FEB-1998
ATTORNEY_AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEPHONE: (612) 305-1228
                                                                                                                                                                                                        TELEFAX: (612) 305-122
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: single
TOOLCGY: linear
                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HORNE, SHELLER APPLICANT: ROBINSON, MICHAEL

TOP INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
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STREET: 11
                                           / Match 100.0%;
Local Similarity 100.0%;
nes 309; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 31-MACLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE:
1 atgcaggataataagatgaaaaaatgttattttctgccgctctggccaatgcttattaca 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tcacaatag 309
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119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HORNE, SHELLEY M.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                       US 09/023,221
                                                                                                                                                                                                                                                                                                                                                                                                                 US/09/282, 352A
                                                                                                                                                                                                                                                                                 255.00010102
                                           Score 309; DB 4;
Pred. No. 7.6e-86;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Version #1.30
                                                                        Length 760;
                                            Indels
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atgcaggataataagatgaaaaaaatgttattttctgccgctctggcaatgcttattaca 60

Conservative

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Indels

2

Gaps

ATGCAGGATAATAAGATGAAAAAAATGTTATTTTCTGCCGCTCTGGCAATGCTTATTACA 60

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US-09-023-221A-5
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US-09-023-221A-5
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 Query Match
Best Local Similarity
Matches 300; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5, Application US/09023221A Patent No. 6087128
                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA;
APPLICATION NUMBER: US/09/023,221A
FILLING DATE: 12-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                    TELEFAX: (612) 305-12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESSE: METING, RAASCH & GEBHARDT P.A.
ADDRESSEE: METING, RAASCH STREET, SUITE 203
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                         SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: MINNEAPOLIS
STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITLE OF INVENTION: DNA ENCODING AN AVIAN E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          É
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                     TOPOLOGY:
                                                                                                                                  STRANDEDNESS:
                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                       ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aaaatttgtggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaaat 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     55401
                                                                                                                                                    nucleic acid
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                                                                                                                       linear
                                                                                                                                                                                                                                         (612)
                                                                                                                                     single
                 96.8%;
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                                                                                                                                                                                                                                                                           255.00010101
Score 273.2; DB 3;
Pred. No. 5.2e-75;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                               Version
                                                                                                                                                                                                                                                                                                                                                                                                               #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLI ISS
                              Length 309;
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61 61

GGATGTGCTCAACAAACGTTTACTGTTGGAAACAAACCGACAGCAGTAACACCAAAGGAA 120 99atgtgotcaacaacgtttactgttggaaacaaaccgacagcagtaacaccaaaggaa

120

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RESULT
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                                              Query Match
Best Local Similarity
Matches 300; Conserva
                                                                                                                                                                                                                      TELEFAX: (612) 305-1228
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US 0
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 22
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                                                                                                                                                                      LENGTH: 309 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010102
                                                                                                                                                                                                                                                                                                                      NAME: SANDBERG MS., VICTORIA A. REGISTRATION NUMBER: 41,287
                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 31-MAR-1999
1 atgcaggataataagatgaaaaaaatgttattttctgccgctctggccaatgcttattaca 60
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ilarity 96.8%;
Conservative
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HORNE, SHELLEY M.
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                                            Score 273:2; DB 4;
Pred. No. 5.2e-75;
0; Mismatches 8;
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                Query Match
Best Local Similarity
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                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                       TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                SEQUENCE CHARACTERISTICS
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                                                                                                                   STRANDEDNESS:
                                                                                                                                  TYPE: nucleic acid
                                                                                                                                                                                                         TELEPHONE:
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E: MUETING, RAASCH & GEBHARDT P.A.
119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                309 base pairs
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                                                                                    DNA (genomic)
                                                                                                                   single
                81.6%;
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Score 252; DB 3; |
Pred. No. 1.7e-68;
0; Mismatches 35;
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Best Local Sim
Matches 273;
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                                                                                                                                                                                                                                                         FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.0001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
                                                                                                                                                                                                              TELEFAX: (612) 305-122
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                  LENGTH: 309 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 3
CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: MINNEAPOLIS
STATE: MN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE:
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 1 atgcaggataataagatgaaaaaaatgttattttctgccgctctggccaatgcttattaca 60
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| TCACAATA 308
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5. 6187321
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                                                            Similarity
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HORNE, SHELLEY M.
ROBINSON, MICHAEL
IVENTION: DNA ENCODING AN AVIAN E. COLI ISS
EQUENCES: 22
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                                                                                                                                     DNA (genomic)
                                                            81.6%;
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                                            Score 252; DB 4; Pred. No. 1.7e-68; 0; Mismatches 35;
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US-09-470-618-13
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Best Local Similarity 88.6%;
Matches 273; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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                                                                                          9415
                                                                                                                                                9355 ggatgtgctcaacagacgtttactgttcaaaaacaaaccggcagcagtagcaccaaaggaa 9414
                                                                                                                                                                                                              9295 atcgggaataacaccatgaaaaaaatgctactcgctactgcgctggccctgcttattaca 9354
                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH: 11933
                                            181 aaaatttgtgggggtgcagaaatgttgttaaaacagaaacctcagcaaaccattcgtaaat 240
                                                                                                       121 accatcactcattcattcgtttcgggaattggacaagagaaaactgttgatgcagcc 180
241 ggattgctcggttttatcacttttggcatctatactccgctggaagcccgggtatattgc 300
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; OTHER INFORMATION: Description of Artificial Sequence: US-09-470-618-13
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TITLE OF INVENTION: by Target Cells
FILE REFERENCE: AVIgen-04082
CURRENT APPLICATION NUMBER: US/09/470,618
CURRENT FILING DATE: 1999-12-22
EARLIER APPLICATION NUMBER: 09/364,862
EARLIER FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
                                                                                                                                                                                                                                                                                                                                     EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                            EARLIER FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Couto, Linda B.
APPLICANT: Colosi, Peter C
                                                                                                                                                       ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 accatcactcattcatttcttcgtttcgggaaattggacaagagaaaactgttgatgcagcc 180
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Score 252; DB 4;
Pred. No. 6.6e-68;
0; M1smatches 35
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                                           Length 11933;
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                                                                                                      US-09-002-361-4
                               Sequence 4, Application Patent No. 6329516
GENERAL INFORMATION:
APPLICANT: Halling,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 273; Conserv
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SEQ ID NO 13
LENGTH: 11933
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
FILE REFERENCE: AVIGEN-03743
CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER FILING DATE: 1999-10-20
RARLIER FILING DATE: 1998-10-20
NUMBER: 05/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER: 05/104,994
EARLIER FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Couto, Linda B. APPLICANT: Colosi, Peter C.
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 TITLE OF
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NT: Halling, F INVENTION: F INVENTION:
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 Lepidopteran GABA-Gated Chloride Channels
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Pred. No. 6.6e-68;
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                                                                                                                                                                                                          Sequence 1, Approximate No. 5994066
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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Best Local Similarity
                                                                                                                                                                                                 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1519 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Bloom, Allen
REGISTON NUMBER: 29,135
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 609-520-3214
                                                                                                                                                                                                                                                                                                                   1052
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                APPLICANT:
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                               CORRESPONDENCE ADDRESS
                                                NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                    213 aacagaaactc
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STREET: 997 Lenox Drive, Building 3,
CITY: Lawrenceville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Coding Sequence LOCATION: 1...1443
OTHER INFORMATION:
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SOFTWARE: FastSEC
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STREET:
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411 EAST WISCONSIN AVENUE
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ROY, Paul H.
                                                                                                                                                                PICARD, Francois J.
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                                                                 ANTIBIOTIC RESISTANCE GENES
                                                                               SPECIES-SPECIFIC AND UNIVERSAL DNA PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/002,361
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                                                                     SPECIMENS
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ZIP: 53202-4497

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Applic
Patent No. 6001564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 10.9%;
Best Local Similarity 51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING LALL.
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PREDE TO THE PROPERTY OF 1997
PRIOR TO THE PROPERTY OF 1995
PRIOR TO 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85
TELECOMMUNICATION INFORMATION:
TELEPHONE: (414) 277-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1331 ATGGGTTATATTATTTCGGGTGCATCTAATCC 1362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1211 ACGTATGCTTCCTCTTTAGATGTAGTTGGTCATGAAATGACACATGGTGTGACGGAACAT 1270
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                  ADDRESSEE: QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 127 actcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagccaaaatt 186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         187 tgtggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaatggattg 246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247 ctcggttttatcacttttggcatctatactcc 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                              Milwaukee
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         INVENTION:
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                                                                                                                                                                                        Wisconsin
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                                                                                                                                                                                                                                                                411 East Wisconsin Avenue
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                                                                                                                                                                                                                                                                                                                                                                                                        SPECIFIC AND UNIVERSAL PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC REFROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSI
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                                                                                                                                                                                                        Query Match 10.9%;
Best Local Similarity 51.3%;
Matches 78; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (414) 277-55 INFORMATION FOR SEQ ID NO:
                                                                  1271
                                                                                                                                       1211 ACGTATGCTTCCTCTTTAGATGTAGTTGGTCATGAAATGACACATGGTGTGACGGAACAT 1270
                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                    127 actcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagccaaaatt 186
                                247 ctcggttttatcacttttggcatctatactcc 278
                                                                                                   187 tgtggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaatggattg 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: BAKER, Jean C.
REGISTRATION NUMBER: 35
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US OF FILING DATE: 12-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM:
SOFTWARE: Patent:
                                                                                                                                                                                                                                                                                                                 ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       relephone:
                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH:
ATGGGTTATATTTTCGGGTGCATCTAATCC 1362
                                                                  : 1817 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                               Enterococcus faecalis
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PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (414)
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277-5591
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                                                                                                                                                                                                        Score 33.6; DB 3;
Pred. No. 0.34;
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Search completed: July 23, 2002, 13:45:10 Job time: 5111 sec

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Listing first 45 summaries
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Match
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1450.239 Million cell updates/sec
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309
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1981_DAT:*
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1983_DAT:*
/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1983_DAT:*
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/SIDS5/gcgdata/geneseq/geneseqn-emb1/NA1993.DAT:
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/SIDS5/gcgdata/geneseq/geneseqn-embl/NA1997.DAT:
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10.3	10.3	10.3	10.3	10.3	10.3	10.3	10.4	10.4	10.4	10.4	10.4	10.4	10.5	10.5	10.6	10.6	10.6	10.6	10.6	10.6	10.7	10.7	10.7	10.9	10.9	10.9	11.1	11.4	11.7	11.7	12.6	45.8	81.6	81.6	81.6
6034	3511	3249	. 3233	2754	1470	1470	73334	344	4963	2364	1690	408	106416	1924	7657	1839	1727	6272	4381	4380	1698	1263	225	5756	1817	1817	1519	4951	3783	1685	1023	180	193	11933	309
23	22	22	22	22	22	22	24	21	22	22	16	21	23	16	20	20	20	18	12	10	21	21	20	23	22	17	20	20	22	21	23	22	22	21	22
ABL12986	AAH54566	AAH54258	AAH54222	AAK80652	AAH53892	AAH53837	ABL34125	AAC21119	AAF77841	AAF77837	AAQ92524	AAZ80085	ABL18718	AAQ80002	AAX12970	AAX20146	AAX20147	AAV74451	AAQ10519	AAN91839	AAC36256	AAC43008	AAX99646	ABL12582	ABA76825	AAT28545	AAV64373	AAX13198	AAC84094	AAA26702	AAS93939	ABA88818	AAD08612	ដ	AAF58788
Drosophila melanog	S. epidermidis gen	epidermidis	S. epidermidis gen	man immune/h	s. epidermidis ope	· epi	uman	Human secreted pro	Fragment of Clostr	Glycerol dehydrata	Nicotiana alata ar	Human colon cancer	Drosophila melanog	ADP-glucose-pyroph	Enterococcus faeca	Enterococcus faeca	Enterococcus faeca	Staphylococcus aur	Pasteurella multoc		Arabidopsis thalia		Nucleic acid seque	Drosophila melanog	Enterococcus faeca	E. faecalis detect	GABA-gated chlorid	Enterococcus faeca	Streptococcus pyog	Candida albicans p	DNA encoding novel	Escherichia coli p		inant adence	Phage lambda bor g

### ALIGNMENTS

RESULT
AAA73698
ID AAA7
XX
AC AAA7
XX

AAA73698;

AAA73698 standard; DNA; 309 BP

07-DEC-2000 (first entry)

Avian Escherichia coli iss cDNA.

Iss; avian; outer membrane protein; OMP; vaccine; antibacterial; avian colibacillosis; septicemic; pGEX-6P-3; ss.

CDS Nolan LK, (NDSU-) NDSU RES FOUND 12-FEB-1998; 11-JUL-2000. US6087128-A. Escherichia coli. 12-FEB-1998; Horne SM; 9805-0023221 98US-0023221 Location/Qualifiers
1..309 /product= Iss

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RESULT
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Best Local S
Matches 309
                                                                                                                                 Avian E coli infection; colibacillosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Is encodes an outer membrane protein. This gene was obtained by PCR amplification of an E.coli isolate from chick serum. The present sequence is the iss cDNA as cloned in frame into the expression vector pGEX-6p-3. The iss gene is useful as a vaccine for treating and preventing avian septicemic diseases and functions as a marker for diseases causing avian E. coli infection. This forms the basis for improved diagnostic and control strategies for avian colibacillosis.
         12-FEB-1998;
                                  31-MAR-1999;
                                                                                                          Escherichia coli
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                                                                                                                                                                                                04-MAY-2001
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                                                          13-FEB-2001.
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P-PSDB; AAB14981.
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                                 9905-0282352
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                                                                                                                                                                      iss gene
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                                                                                                                                            respiratory tract lesion; septicaemia;
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                                                                                                                                                                      clone
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Pred. No. 8.4e-80;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the avian Escherichia coli
                                                                                                                                                                      SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 21;
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О:
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Best Local
                                                                                       avian
                                                                                                                E.coli iss gene in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Escherichia coli Iss protein. This can be used in the diagnosis and treatment of, and vaccines against, E. coli infection in domestic bir where the bacterium causes septicaemia, respiratory tract lesions and colibacillosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     useful for treating -- colibacillosis, coligranuloma,
                                                                                                                                  07-DEC-2000
                                                                                                                                                     AAA73697;
                                                                                                                                                                      AAA73697 standard;
                                                                       Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                      colibacillosis;
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                                                                     coli
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nilarity 100.
Conservative
                                                                                              outer membrane protein;
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                                           Location/Qualifiers 34..342
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                                                                                                                expression vector pGEX-6P-3.
                                                                                                                                                                      DNA;
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                                                                                      septicemic;
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Pred. No. 8.4
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peritonitis, salpingitis,
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                                                                                     n; OMP; vaccino
pGEX-6P-3; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 84 T; 0 other;
                                                                                              vaccine;
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9.4e-80;
9s 0;
                                                                                              antibacterial;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acid molecule encoding Iss polypeptide isolated from Escherichia coli, used to prevent avian septicemic diseases diagnostic and control strategies for avian colibacillosis
                                                                                                  04-MAY-2001
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               colibacillosis;
                             Avian E coli infection; respiratory tract lesion; septicaemia
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nes 309; Conserv
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DB; AAB14984.
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                                                                 col1
                                                                                                                                                                   standard;
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llarity 100.0%;
Conservative (
                                                                                                (first
                                                               isolate protease cleavage site
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                                                               DNA SEQ
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated and purified avian Escherichia coli Iss polypeptide useful for treating Escherichia coli infection selected from colipacillosis, coligranuloma, peritonitis, salpingitis, synovitis
                        Avian Escherichia
                                              07-DEC-2000
                                                                     AAA73681;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                             (first entry)
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                       coli iss
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Pred. No. 8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 22;
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diagnosis
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Query Match
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Matches 309; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the avian Escherichia coli iss gene. Iss encodes an outer membrane protein. This gene was obtained by PCR amplification of an E.coli isolate from chick serum. The primers used are shown in AAA73682 and AAA73683. The iss gene is useful as a vaccine for treating and preventing avian septicemic diseases and functions as a marker for diseases causing avian B. coli infection. This forms the basis for improved diagnostic and control strategies for avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid molecule encoding Iss polypeptide isolated from avi
Escherichia coli, used to prevent avian septicemic diseases and
diagnostic and control strategies for avian colibacillosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                     ggatgtgctcaacaaacgtttactgttggaaacaaaccgacagcagtaacaccaaaggaa
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                                                                                                                                   aaaatttgtggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaaat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-531343/48.
DB; AAB14981.
                                                tcacaatag 309
                                                                                                                      aaaatttgtggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaat
                                                                                                                                                                      accatcactcatcattcttcgttttcgggaattggacaagagaaaactgttgatgcagcc
                                                                       ggattgctcggttttatcacttttggcatctatactccgctggaagcccgggtatattgc
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/product- "iss"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Avian E coli infection; respiratory tract lesion; colibacillosis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 760 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present invention provides the protein and coding sequences of the Escherichia coli Iss protein. This can be used in the diagnosis and treatment of, and vaccines against. E. coli infection in domestic birds, where the bacterium causes septicaemia, respiratory tract lesions and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31-MAR-1999;
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tcacaatag 309
                                                                              ggattgctcggttttatcacttttggcatctatactccgctggaagcccgggtatattgc
                                                                                                                                                           aaaatttgtggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaaat
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DB; AAB69394.
                                                                                                                                      aaaatttgtggcggtgcagaaaatgttgttaaaaacagaaactcagcaaacattcgtaaat
                                                                                                                                                                                                                       accatcactcattcttcgtttcgggaattggacaagagaaaactgttgatgcagcc
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                                                         ggattgctcggttttatcacttttggcatctatactccgctggaagcccgggtatattgc
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Pred. No. 1.1e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            160 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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Matches 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     avian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA73684
                                                                                                                                                                                                                                                                                                        Nucleic acid molecule encoding Iss polypeptide isolated from avian Escherichia coli, used to prevent avian septicemic diseases and for diagnostic and control strategies for avian colibacillosis
                                                                                                                                                                                                                                                                                                                                                                                                                                      11-JUL-2000
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                                                                                                                                                                                Sequence
                                                                                                                                                                                                septicemic diseases and functions as a marker for diseases causing avian E. coli infection. This forms the basis for improved diagnostic and control strategies for avian colibacillosis.
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        aaaatttg-tggcggtgcagaaaatgttgttaaaacaggaaactcagcaaacattcgtaaa
                                        accatcactcatcatttcttcgtttcggggaattgggacaagggaaaactgttgatgcagcc
                                                                          gyatytyctcaaccaaccytttactyttgyaaacaaaccgyacagcagtaacaccaaaggaa
                                                                                                   atgcaggataataagatgaaaaaaatgttattttctgccgctctggcaatgcttattaca
                                                                                                           atgcaggataataagatgaaaaaaatgttattttctgccgctctggccaatgcttattaca
aaaatttgttggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaa
                                 accatcactcatttcttcgtttccccaattggac-agagaaaactgttgatgcagcc
                                                                 ggatgtgctcaacaaacgtttactgttggaaacaaaccgacagcagtaacaccaaaggaa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    colibacillosis;
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                                                                                                                                                                                 309
                                                                                                                                                                                             coll infection. This infection of avian
                                                                                                                                                                                                                                                                                                                                                                   Horne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   coli.
                                                                                                                                                                                                                                                                                       Fig 1; 33pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             outer membrane
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                                                                                                                                                                                101 A; 65 C;
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                                                                                                                                              96.8%;
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                                                                                                                                     Score 273.2; Pred. No. 1.9e 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated and purified avian Escherichia coli Iss polypeptide useful for treating Escherichia coli infection selected from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Avian E coli infection; respiratory tract lesion; colibacillosis; ds.
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                                                                                                                                                                                                                                                                                                             Sequence 309 BP;
                                                                                                                                                                                                                                                                                                                                             colibacillosis.
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aaaatttg-tggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaaa
                                                           accatcactcattcttcttcgtttcggggaattgggacaagagaaaactgttgatgcagcc
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                                             accatcactcatcatttcttcgtttccccaattggac-agagaaaactgttgatgcagcc
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96.8%;
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Pred. No. 1.
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                                                                                                                                                                                                                                                                                                              59 G;
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                                                                                                                                                                                                                                  Mismatches
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Matches 273
                                                                                                                                                The present invention relates to the avian Escherichia coli iss gene. Iss encodes an outer membrane protein. This gene was obtained by PCR amplification of an E.coli isolate from chick serum. The present sequence is the lambda bor gene, which shows homology to the avian E. coli iss gene. The iss gene is useful as a vaccine for treating and preventing avian septicemic diseases and functions as a marker for diseases causing avian E. coli infection. This forms the basis for improved diagnostic and control strategies for avian colibacillosis.
                                                                                                                                                                                                                                                                                Nucleic acid molecule encoding Iss polypeptide isolated from avian Escherichia coli, used to prevent avian septicemic diseases and for diagnostic and control strategies for avian colibacillosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CDS
                                                                                                                                                                                                                                                            Disclosure; Fig 1; 33pp; English.
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ggatgtgctcaacaaacgtttactgttggaaacaaaccgacagcagtaacaccaaaggaa
                    atcgggaataacaccatgaaaaaatgctactcgctactgcgctggccctgcttattaca
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colibacillosis; septicemic; lambda;
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                                                                     Similarity 88.0
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                                                                                                                                                                                                                                                                                                                                                                  Horne SM;
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                                                                                                                               69 C; 65 G;
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                                                                    Score 252; DB 21;
Pred. No. 2.5e-63;
0; Mismatches 35;
                                                                                                                              78 T; 0 other;
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; bor; ds.
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Query Match
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Matches 273; Conserv

Conservative

81.6%; 88.6%;

Score 252; DB Pred. No. 2.5e 0; Mismatches

DB 22; 5e-63;

Length 309; Indels

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                          The present invention provides the protein and coding Escherichia coli Iss protein. This can be used in the treatment of, and vaccines against, E. coli infection where the bacterium causes septicaemia, respiratory tr
                                                                                                       Novel isolated and purified avian Escherichia coli Iss polypeptide useful for treating Escherichia coli infection selected from colibaciliosis, coligranuloma, peritonitis, salpingitis, synovitis omphalitia
                   colibacillosis.
                                                                                Example 1;
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                                                                                                                                                                           Nolan LK, Horne
                                                                                                                                                                                                                     12-FEB-1998;
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                                                                                                                                                                                                                                                                                                                         Avian E coli infection; colibacillosis; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                    standard; DNA;
                                                                                Column 39-40;
                                                                                                                                                                                                                                                                                                                                                       bor gene SEQ ID
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                                  agnosis and
domestic birds
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The present DNA sequence is a recombinant adenovirus-associated vector, (rAAV) construct, pAAV-F8-1. This expression vector comprises the HNF-3 albumin promoter, the first intron (-573 to +985) of human elongation factor-lalpha (EFIAlpha) gene, human Factor VIII coding sequence (hFVIII) and polyadenylation signal from human growth hormone (hGH). This sequence is inserted between the AAV inverted terminal repeat (ITR) regions. The hFVIII coding region comprises the heavy chain gene segment with the first 57 bp encoding the 19 amino acid signal peptide, A1 and A2 domains and 5 amino acids from the N-terminus of the B domain. The light chain segment comprises the C-terminal 85 amino acids of B domain and the A3, C1 and C2 domains. Both the heavy and light chain segments are cloned into the same plasmid seperated by 42 nucleotides coding for 14 residues of the B domain, that is deleted. This plasmid is operably linked to
                                                                                                                                                                                                                                          New recombinant adenovirus-associated vector, useful for gene therapy to treat hemophilia, comprises at least a portion of Factor VIII operably linked to control sequence -
                                                                                                                                                                                                                Example 2;
                                                                                                                                                                                                                                                                                                         WPI; 2000-339536/29.
                                                                                                                                                                                                                                                                                                                                       Couto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAD00121 standard;
                                                                                                                                                                                                                                                                                                                                                                (AVIG-) AVIGEN INC.
                                                                                                                                                                                                                                                                                                                                                                                                 30-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                             20-OCT-1998;
24-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200023116-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Adeno associated virus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAD00121;
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99US-0125974.
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                                                                                                                                                                                                                English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ctor; rAAV; pAAV-F8-1; human Factor VIII;
human elongation factor-lalpha; EF1alpha;
rted terminal repeat; ITR; haemophilia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        construct,
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Best Local S
Matches 273
                                                                                                                                                                                     Chimeric
Chimeric
Chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Factor VIII gene. The adeno-associated viral vectors are used for gene therapy to treat haemophilia. This method allows prolonged expression therapeutic levels of Factor VIII in vivo. The rAAV are used for gene therapy, because of their broad host range, safety profile and duratic of expression in the infected hosts.
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                       WPI; 2001-417955/44.
                                             Couto
                                                                                                                                                                                                                        Chimeric -
                                                                                                                                                                                                                                             Recombinant adeno-associated viral vector; rAAV; factor VIII; FVIII; blood clotting disorder; gene therapy; haemophilia A; human; pAAV-F8-1; ds.
                                                                                                                                                                                                                                                                                            Human factor VIII expressing rAAV vector pAAV-F8-1 partial sequence.
                                                                                                                                                                                                                                                                                                                                                                 AAD08612 standard;
                                                                                          22-DEC-1999;
                                                                                                                21-DEC-2000;
                                                                                                                                       28-JUN-2001
                                                                                                                                                                                                                                                                                                                                           AAD08612;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            control sequences, Factor VIII gene.
                                                                  (AVIG-)
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                                            Colosi PC,
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                                                                                                                                                                                                                                                                                                                                                                   11933
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.5e-63;
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Best Local Similarity
Matches 273; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          second recombinant adeno-associated virion comprising a nucleotide sequence encoding the heavy chain of factor VIII. The rAAV vector is useful in gene therapy for treating haemophilia A in mammals, in particular humans. The rAAV vector provides high level and long term expression of biologically active clotting factor VIII in vivo. The present sequence is pAAV-68-1 vector without the plasmid backbone. It comprises HNF-3 mouse albumin promoter, a synthetic introbased on human elongation factor lalpha (EFlalpha) and immunoglobulin (19G) intron sequences, B-domain deleted human factor VIII coding sequence, poly A signal based on rabbit beta-globin sequence and AAV inverted terminal repeats (ITRs) at the ends. The vector encodes both light and heavy chains of human factor VIII.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a method for treating a subject suffering from a blood clotting disorder. The method comprises
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                                                                                                immunosuppressive; extra-intestinal infection; systemic infection; non-diarrhoeal infection;
                                                                                                                                                                                                  11-FEB-2002
                                                                                                                                                                                                                                    ABA88818;
                                               Escherichia coli
                                                                                pyelonephritis;
                                                                                                                                   Escherichia
                                                                                                                                                                 Escherichia
                                                                                                                                                                                                                                                                     ABA88818 standard;
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                                                                                  antibiotic
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Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                 SEQ ID NO 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2717 G; 3140 T;
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7.5e-63;
hes 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 11933;
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WO200166572-A2.

30-MAR-2001; 2001WO-US08631

11-OCT-2001. WO200175067

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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a library of DNA fragments of Escherichia coll strains comprising polynucleotides (ABA88577-ABA88729 and ABA89533) and encoded proteins (ABB52459-ABB52919 and ABB5294-ABB53094) of nature B2/D+A-. The polynucleotides have potential antiinflammatory, antibacterial and immunosuppressive activity as part of pharmaceutical compositions used to treat, pallate or prevent extra-intestinal E. coll infections. The polypeptides are useful for determining the phylogenic group of a given E. coll strain. These polypeptides can detect and treat an undesired development of E. coll; particularly an extra-intestinal infection that include systemic and non-diarrhoeal infections such as septicaemia, pyelonephritis and meningitis this is particularly advantageous as bacterial resistance is increasing with the more frequent use of broad spectrum antibiotics.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A library of DNA fragments of Escherichia coli strains for the phylogenic determination of a given strain comprises polynucle
                                                                                                                                                                                                             AAS93939
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02-FEB-2001; 2001FR-0001449.
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                                                                                                                                                                                 13-FEB-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 2; 646pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INRM ) INSERM INST NAT SANTE &
                                                                              Homo sapiens
                                                                                                                                                   DNA encoding novel human diagnostic protein #29743.
                                                                                                         food supplement;
                                                                                                                        Human;
                                                                                                                                                                                                                                                                                                                                          121
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                                                                                                                                                                                                                                                                                                                            accatcactcatttcttcgtttcggg 149
                                                                                                                                                                                                                                                                                                                                                                                                                            ### ATGCAGGATAATAAGATGAAAAAAATGTTGTTTTCTGCCGCTCTGGCAATGCTTATTACA
                                                                                                                                                                                                                                                                                                                                                                                     GGATGTGCTCAACAGACGTTTACTGTTGGAAACAAACCNACAGCAGTAACACCAAAAGGAA
                                                                                                         chromosome mapping; gene ma
upplement; medical imaging;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         180 BP; 50 A; 35 C;
                                                                                                                                                                                                                                         standard; cDNA; 1023 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bonacorsi S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45.88;
96.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clermont 0,
                                                                                                                        gene mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 141.6;
Pred. No. 1.8e
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39 G; 55 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RECH MEDICALE
                                                                                                           apping; gene therapy;
.diagnostic; genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc polypeptide (II) sequences. (I) is useful as hybridisation probes, cc polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II) The CC polynucleotides are also used in diagnostics as expressed sequence tags of or identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as CC a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics, forensics, gene mapping, identification of mutations in CC diagnostics of genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC anino acid sequences. AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC specification, but was obtained in electronic format directly from WIPO at fit, wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Matches 45; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                                                                                 Candida albicans.
                                                                                                                                                                 Candida albicans infection;
                                                                                                                                                                                                 Candida albicans polynucleotide sequence #40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                 23-DEC-1998;
                                                01-MAR-2000
                                                                                EP982401-A2
                                                                                                                                                 vulvovaginitis;
                                                                                                                                                                                                                                     23-JUN-2000
                                                                                                                                                                                                                                                                       AAA26702;
                                                                                                                                                                                                                                                                                                                                                                                         1022 TACTCGCTACTGCCCTGCCTGCTTATTACAGGATGTGCTCAACAGACATTTAC 968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1023 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                     AAA26702 standard; cDNA; 1685
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DB; ABG29752.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                   (first entry)
                98EP-0310694.
                                                                                                                                                 s infection; growth; survival; medicament;
immunocompromised patient; treat; ss.
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Pred.
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This sequence represents a polynucleotide sequence encoding a polypeptide that is critical for the survival and growth of Candida albicans. The C. albicans sucleic acid molecules of the invention may be used as probes and primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the preparation of a medicament to treat C.albicans associated diseases, especially in AIDS patients and to treat culticans vulvovaginitis in otherwise healthy females. The use of the polypeptides and polynucleotide sequences to treat C.albicans associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for the polypeptides and the treat challenges are separated associated associated associated associated associated associated associated as the polypeptides and polynucleotide sequences to treat C.albicans associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially immunocompromised subjects, e.g., AIDS patients -
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 78; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-258614/23.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JANC ) JANSSEN PHARM NV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-AUG-1998;
                                             immunocompromised patients, such as AIDS patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RH,
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Sequence 1685 BP; 650 A; 281 C; 250 G; 504 T; 0 other;

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                                         20
                                                           Query Match
Best Local S
Matches 62
                          1334
        169
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gttgatgcagccaaaatttgtggcggtgcagaaaatgttgttaaa 213
                        acaccaaaggaaaccatcactcatcatttcttcgtttcgggaattggacaagagaaaact 168
                                                                     11.7%;
                                                            0,
                                                           Score 36.2; DB
Pred. No. 1;
0; Mismatches
                                                                             21;
                                                            43;
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                                                            Indels
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Search con Job time: completed: July 23, 2002, 13:51:29 밁

1394 agtgatgatgagttttattctgatgaagaagatgaagatattgaa 1438

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Result Query
No. Score Match Length DB ID
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Database :
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                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-738-599-22
309
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3317.038 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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gb_htg:*
gb_in:*
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## ALIGNMENTS

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BASE COUNT ORIGIN	FEATURES Source	TITLE JOURNAL	AUTHORS	REFERENCE		ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION	DEFINITION	LOCUS	AR102880	1
/organism="unknown" 101 a 60 c 64 g 84 t	Location/Qualifiers 1. 309	DNA encoding an avian E. coli iss Patent: US 6087128-A 22 11-JUL-2000;	Nolan, L.K. and Horne, S.M.	1 (bases 1 to 309)	Unclassified.	Unknown.	Unknown.		AR102880.1 GI:12814468	AR102880	Sequence 22 from patent US 6087128.	AR102880 309 bp DNA	,	
	٠											linear		
						•						PAT 14-FEB-2001		

Query Match Best Local Similarity

100.0%;

Score 309; DB 6; Length 309; Pred. No. 2.6e-68;

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aaaatttgtggcggtgcagaaaatgttgttaaaacagaaacctcagcaaacattcgtaaat
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309; Conservative 0;
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Sequence 22
AR129424
AR129424.1
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Nolan, L.K., Horne, S.M. and Robinson, M. Avian E. coli Iss polypeptide
Patent: US 6187321-A 22 13-FEB-2001;
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Nolan,L.K. and Horne,S.M.

Nolan,L.K. and Horne,S.M.

Nolan,L.K. and Horne,S.M.

Nolan,L.K. and Horne,S.M.

Patent: US 6087128-A 21 11-JUL-2000;

Location/Qualifiers

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Nolan, L.K., Horne, S.M. and Robinson, M. Avian E. coli Iss polypeptide
Patent: US 6187321-A 21 13-FEB-2001;
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/gence"189" /notes"81milar to Bacteriophage lambda Bor protein, and to Iss protein from a septicemic human Escherichia coli isolate; causes avian colibacillosis" /codon_start=1 /transl_table=11 /product="Iss" /protein_id="AAD41540.1" /db_xref="GI:5305230" /translation="MODNINKKMLFSAALAMLITGCAOOTFTVGNKPTAVTPKETITH	FEATURES  Location/Qualifiers  source  /organism="Escherichia coli" /strain="102" /strain="102" /db_xref="taxon:562" /note="may be on a large R plasmid"  gene  292600 /gene="iss" CDS /22600		Oy 121 accatcactcatcattctttcgggaattggacaagagaaactgttgatgcagcc 180	Query Match Query Match 100.0%; Score 309; DB 6; Length 378; Best Local Similarity 100.0%; Pred. No. 2.6e-68; Matches 309; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  Oy 1 atgcaggatastasgatgasasastyttatttctgccgctctggcastgcttattaca 60
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Nolan, L.K., Horne, S.M. and Robinson, M.
Avian E. coli Iss polypeptide
Patent: US 6187321-A 1 13-FEB-2001;
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1 (bases 1 to 309)

Nolan,L.K., Horne,S.M. and Robinson Avian E. coll Iss polypeptide Patent: US 6187321-A 5 13-FEB-2001;
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DNA encoding an avian E. coli iss
Patent: US 6087128-A 5 11-UUL-2000;

Location/Qualifiers
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nilarity 96.8%;
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0; Mismatches 8
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1 (bases 1 to 1430)

Chuba, P.J., Leon, M.A., Banerjee, A. and Palchaudhuri, S.

Cloning and DNA sequence of plasmid determinant iss, codin
increased serum survival and surface exclusion, which has
with lambda DNA
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89313666
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81.6%;

Score 252; DB 6; Pred. No. 7.6e-54; 0; Mismatches 35

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1 (bases 1 to 309)
Nolan,L.K. and Horne,S.M.
Nolan,L.K. and Horne,S.M.
DNA encoding an avian E. coli iss
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Nolan,L.K., Horne,S.M. and Robinson,M. Avian E. coll Iss polypeptide
Patent: US 6187321-A 6 13-FEB-2001;
Location/Qualifiers
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GGATGTGCTCAACAGACGTTTACTGTTCAAAACAAACCGGCAGCAGTAGCACCAAAGGAA 128
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1 (bases 1 to 326)
Barondess, J.J. and Beckwith, J.
A bacterial virulence determinant encoded
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/codon_start=1
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GIGQKKTVDAAKICGGAENVVKTETQQTFVNGLLGFITLGIYTPLEARVYCSQ"
72 c 69 g 81 t
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24. .317
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/db_xref="taxon:10710"
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                                                                                                                                                                                                                                                                                                                                                                                                  Cloning vector lambae artificial sequence; 1 (bases 1 to 9170)
                                                                                           Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc., 1020 East Meadow Circle, Palo Alto, CA 94303, USA
This sequence has been compiled from information in the sequence databases, published literature and other sources. If you suspect there is an error in this sequence, please contact CLONTECH's Technical Service Department at (415) 424-8222 or (800) 662-2566, extension 3 or E-mail TECH@CLONTECH.COM.
                                                                                                                                                                                                                                                                                 2 (bases 1 to 9170)
Frischauf, A.M., Lehrach, H., Poustka, A. and Murray, N.
Lambda replacement vectors carrying polylinker sequences
J. Mol. Biol. 170 (4), 827-842 (1983)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cloning vector lambda
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                                                                                                                                                                                                                                                                                                                                                      Unpublished
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              /organism="Cloning vector lambda
/db_xref="taxon:31783"
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7170 TCACAATA 7163
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Cloning vector lambda EMBL3 SP6/T7,
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U02427.1 GI:413793
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Cloning vector lambda EMBL3 SP6/T7
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Direct Submission
Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
Submitted (07-OCT-1993) Paul A. Kitts, CLONTECH Laboratories, Inc.,
1020 East Meadow Cirice, Palo Alto, CA 94303, USA
1020 East Meadow Cirice, Palo Alto, CA 94303, USA
1020 East Meadow Cirice, Palo Alto, In the sequence
This sequence has been compiled from information in the sequence
databases, published literature and other sources. If you suspect
there is an error in this sequence, please contact CLONTECH's
there is an error in this sequence, please contact CLONTECH's
Technical Service Department at (415) 424-8222 or (800) 662-2566,
extension 3 or E-mail TECH@CLONTECH.COM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLONTECH Vectors On Disc version 1.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 artificial sequence;
1 (bases 1 to 9205)
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milarity 88.6%;
Conservative
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/db_xref="taxon:31784"
2002 c 2253 g 2404 t
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Pred. No. 6.4e-54;
0; Mismatches 35;
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BE493915 WHE1276_B
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ALISO728 Tetracdon BM258478 523288 MA AV618307 AV618307	ALIO276 Drosophil BI745078 rk95hl0 y AA842275 MBAFCW6D1 ALIO276 Drosophil ALIO276 TST6158			AZ539756 ENTGJ95TR AV532310 AV532310 AV537481 AV537481 AZ927608 476. dkt27 BM168198 EST570721 B88032 RPC111-17F1 AZ575735 AZ3PSF10

ALIGNMENTS

RESULT 1
AW619529/c
LOCUS
DEFINITION
ACCESSION
VERSION
VERSION
KEYWORDS ORGANISM source FORWARD: GGAAACAGCTATGACCATG
BACKWARD: GTAAAACGACGGCCAGT
Seq primer: AATTAACCCTCACATAAAGGG.
Location/Qualifiers Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt\_trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -minmatch 12 options. Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 332) Smith.T.P.L., Fahrenkrug, S.C., Rohrer, G.A., Simmen, F.A., Rexroad, C.E. and Keele, J.W. AW619529 332 bp, 7594 MARC PBE Sus scrofa cDNA 5', AW619529 1 GI:7325713 Mapping of expressed sequence tags from a porcine early embryonic PCR PRimers 21314990 scrofa library Genet. 32 (2), /organism="Sus scrofa"
/db\_xref="taxon:9823"
/clone\_lib="MARC PBE"
/tissue\_type="Day 12 whole embryos"
/lab\_host="XLOLR" 66-72 (2001) mRNA sequence. linear EST 24-MAR-2000

/note="vector: pBLUESCRIPT SK-; Site\_1: EcoRI; Site\_2:
khoI; Library made from pool of embryos in spherical and

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AV398499
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grgrgrarrgcrcacaataatrgc 69
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV398499 MRNA linear ES
AV398499 Bombyx mori ovary BmNPV infected; 2 hr after
Bombyx mori cDNA clone NV021882 T3, mRNA sequence.
AV398499
                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Bombycoidea; Bombycidae; Bombyx.

1 (bases 1 to 731)

Mita,K., Morimyo,M., Shimada,T., Okano,K. and Maeda,S.
Bombyx mori cDNA
Unpublished (2000)
                                                                                                                                                                                                   Project-'Silkworm Genome Program in MAFF, and Research for Future Program in JSPS'. see 'SilkBase', <a href="http://www.ab.a.u-tokyo.ac.jp/silkbase/">http://www.ab.a.u-tokyo.ac.jp/silkbase/</a>, for whole ESTdb.
                                                                                                                                                                                                                                                                                          Genome Research Group
National Institute of Radiological Sciences
Anagewa 4 9-1, Inage, Chiba 263-8555, Japan
Email: kmita@nirs.go.jp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bombyx mor1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           domestic silkworm.
                                                                                                                                                                                                                                                                          method:uni-directional, sequence direction:sequenced from T3 primer
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8 C 74 g 96 t
          /tissue_type="ovary"
/cell_type="BmN cultured cell"
/dev_stage="BmNPV infected; 2 hr
171 c 164 g 202 t
                                                                                                                   /organism="Bombyx mori"
/db_xref="taxon:7091"
/clone="NV021882"
                                                                                                                                                                                   Location/Qualifiers
                                                                                 inoculation*
                                                                                                   /clone_lib="Bombyx mori ovary BmNPV
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Pred. No. 9.2e-55;
0; Mismatches 20
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Best Local Similarity
Matches 198; Conserv
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97104 MARC 1BOV Bos taurus cD
AW659631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 240)

Smlth, T.P.L., Grosse, W.M., Freking, B.A., Roberts, A.J., Stone, R.T., Casas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C., Bennett G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A., Chitko-Mokown, C.G. Pertea, G., Holt, I., Karamycheva, S., Liang, F., Quackenbush, J. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel: 402 762 4366 Fax: 402 762 4390
                                                                                                                                                                                       BACKWARD: GTTTTCCCAGTCACGACG
Plate: 68 row: N column: 3
Seq primer: ATTTAGGTGACACTATAG.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AW659631.1
                                                                                                                                                                                                                                                                                                                    Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscor
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genome Res. 11 (4), 626-630 (2001)
21180013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota;
Mammalia;
                                                                                                                                                                                                                                                                    FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                    PCR PRimers
                                                                                                                                                                                                                                                                                                       and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence evaluation of four pooled-tissue normalized bovine cDNA lbraries and construction of a gene index for cattle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovidae; Bovinae;
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                  70
              /note-"Vector: pCMV SPORT6; Site_1: xbaI; Site_2: XhoI; Library made from pooled tissue from lymph node, ovary, fat, hypothalamus, and pituitary."

51 c 52 g 67 t
                                                                                                                      /organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 1BOV"
                                                                                     /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Metazoa; Chordata; Craniata; Vertebrata; Eutheria; Cetartiodactyla; Ruminantia; Pec
                                                                                                                                                                            . 240
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Pred. No. 4.3e-42;
0; Mismatches 18
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                                                                                                                                                                                                                                                                                                                         -minscore 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ,c.G.,
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Query Match Best Local Similarity

38.0%;

Score 143.8; DB 9; Pred. No. 5.6e-30;

Length 240;

Matches

240 176

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Best Local Similarity 78.0 Matches 199; Conservative
                                                                                                                                                                                                                                          255 TAATACGACTCNCTATANGGCNAATTTGGTACCGGNCCCCCTGCCTANTACAGGAAGNTC
                                                                                                                                                                                                                                                                  42 taataagatgaaaaaatgttattttctgccgctctggcaatgcttattacaggatgtgc 101
                                                                                                                                                                tttgtggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaaatggat
                                                                                                                 | tcactcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagccaaaa
                      TTTGTGGCGCGCAGAAAATGTTGTTAAAACAGAAACCCAGCAAACATTCGTAANANGAT
                                                                                            TCACCCATCATTTCTTCGTTTCTGGAATTGGGCAGAAAAAACTGTCGATGCAGCCAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TAGGCATTTATACTCCCCTGGAAGCGCGTGTATTGCTCCCAATAATTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tttcgggaattggacaagagaaaactgttgatgcagccaaaatttgtggcggtgcagaaa 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ttggcatctatactccgctggaagcccgggtatattgctcacaatagttgc 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGTTGTTAAAACAGAAACCCACCAAACATTCGTAAATGGATTGCTCGGTTTTATTACTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTTCTGGAATTGGGCAGAAGAAAACTGTCGATGCAGCCAAAATTTGTGGCGGCGCAGAAA 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   University of Washington.
Department of Molecular Biotechnology, Box 357730, University
Washington, Seattle, WA 98195
Tel: 5106280100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI547008 785 bp PN2.1_13_C01.r mynorm Homo sapiens AI547008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prostate cancer (Genomics 59 (2),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: huanggm@yahoo.com.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Guyang Matthew Huang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eroy Hood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           karyota, Metazoa, Chordata, Craniata
mmalia, Eutheria, Primates, Catarrhi
(Dases 1 to 785)
ang,G.M., Ng,W.l., Farkas,J., He,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5106280108
                                                                                                                                                                                                                                                                                                                                                                                                                        prostate t
                                                                                                                                                                                                                                                                                                                                                                                                                      CDNA library was constructed using Lambda ZP II (Stratagene). mRNA was extracted from a frozen prostate tissue (Mayo Clinic)."
128 c 147 g 229 t 128 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="mynorm"
/note="Organ: Prostate; Vector: pBluescript; Directional
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                                                                                                                                                                                                                                                                                                                                 37.0%;
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Pred. No. 9.5e-29;
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5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                Length 785;
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                                                                                                                                                                                                                                                                                                                               tyctcaacaacgtttactyttyyaaacaaaccyacaytaacacccaaayyaaaccat 158
                                                                                                                                                                TTGGGGCGGAGGAAA 206
                                                                                                                                                                                              ttgtggcggtgcaga 233
                                                                                                                                                                                                                                                         cactcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagccaaaat 218
                                                                                                                                                                                                                                                                                                                                                                                  GAATAACACCATGAAAAAAATGCTACTCGCTACTGGCTTGGCCCTGCTTATTACAGGATG 72
                                                                                                                                                                                                                                                                                                                                                                                                       ggataataagatgaaaaaaaatgttattttctgccgctctggcaatgcttattacaggatg 98
                                                                                                                                                                                                                                    CACCCATCATTTCTTCGTTTCTGGAATTGGGC-AGAGAAACCTGTGGTGCAGCCAAAATT 191
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BG895793
359430 MARC
BG895793
BG895793.1
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: om9330@okt.affrc.go.jp
PROJECT - Citrus Genome Analysis
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      National Institute of Fruit Tree Science, Okitsu, Shimizu, Shizuoka 424-02, Japan Tel: +81-543-69-2111 Fax: +81-543-69-2115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hisada,S., Akihama,T., Endo,T., Moriguchi,T. and Omura,M. Expressed sequence tags of Citrus fruit during rapid cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Sapindales; Rutaceae; Citrus.

1 (bases 1 to 223)
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C22108 thyagawa-wase satsuma mandarin orange (
unshiu cDNA clone pcMFRI719.66, mRNA sequence.
C22108
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                                                   93 160 bp
MARC 1PIG Sus scrofa cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="juice sac and pulp segment"
/dev_stage="rapid developing stage"
50 c 52 g 51 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Citrus unshiu"
/strain="Miyagawa-wase satsuma mandarin"
/db_xref="taxon.55188"
/clone="pcMFRI719.66"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="Miyagawa-wase satsuma mandarin
)"
                    GI:14306034
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Pred. No. 2.3e-24;
""" amatches 37;
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REFERENCE AUTHORS

COMMENT

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FEATURES

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SOURCE ORGANISM

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ccaaaatttgtggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaa 271
                                                                                                                                                                                                                                                                                                                                     gctcacaatagttgc 346
                                                                                                                                                                                                                                                                                                                                                                                      ATGGATTGCTCGGTTTTATTACTTTAGGCATTTATACTCCGCTGGAAGCGCGTGTGTATT
                                                                                                                                                                                                                                                                                                                      GCTCACAATAATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tel: 402 762 4366
Fax: 402 762 4390
Email: `smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                               BG835172 160
353618 MARC 1PIG Sus scrofa c
BG835172 BG835172.1 GI:14201080
EST:
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Seq primer: ATTTAGGTGACACTATAG
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stone, R.T., Heaton, M.P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FORWARD: AGGAAACAGCTATGACCAT
BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fahrenkrug, S.C.,
                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 160)
Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dammalia;
                                 and
Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DA, ARS, US Meat Animal Research Center Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nmalia; Eutheria; (bases 1 to 160)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     scrofa
                                 Keele, J.W.
                                                                                                                               scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    iscovery in swine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_11b="MARC 1PIG"
/tlssue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: pCMV SPORT6; Site Library made from pooled tissue and 30 embryos."

37 c 31 g 46 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31.9%;
93.3%;
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on,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 120.6; DB 10; Pred. No. 1.7e-23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                   cDNA 5', mR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               site_1: XbaI;
ssue from day
                                                                                                                                                                                                                     mRNA sequence
                                               ,G.A., Smith,T.P.L.,
Bennett,G.A., Laegre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Site_2:
11, 13,
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Sus.
                                                                                                   Euteleostomi;
Sus.
                                                 Laegreid, W.W.
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15, 20,
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                                                                  Casas, E.,
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JOURNAL COMMENT
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COMMENT
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AUTHORS
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ORGANISM
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BI338974/c
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                                                                                                                                                          TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                    40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCBABATTTGTGGCGGCGCAGAAAATGTTGTTATAACAGAAACCCAGCAAACATTCGTAA 101
                                                                                                                                                                                                                                                                                                                                                                                                                                 gctcacaatagttgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATGGATTGCTCGGTTTTATTACTTTAGGCATTTATACTCCGCTGGAAGCGCGTGTGTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atggattgctcggttttatcacttttggcatctatactccgctggaagcccgggtatatt 331
                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCACAATAATTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BACKWARD: GTTTTCCCAGTCACGACG
Plate: 116 row: L column: 23
Seq primer: ATTTAGGTGACACTATAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Single pass sequencing. Bases ov v0.980904.e. Vector identified and minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USTel: 402 762 4366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PCR PRimers
           Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt_trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore
                                                        USDA, ARS, US Meat Animal PO Box 166, Clay Center, N Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                             Unpublished (2000)
Contact: Smith TPL
                                                                                                                                                                       Stone, R.T., Heaton, M.P., and Keele, J.W.
                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; 1 (bases 1 to 162)
                                                                                                                                                                                                                                                          Sus scrofa
                                                                                                                                                                                                                                                                                                     BI338974.1
                                                                                                                                                                                                                                                                                                                  BI338974
                                                                                                                                                                                                                                                                                                                               162
363710 MARC 1PIG Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                       Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                  Fahrenkrug, S.C., Freking, B.A., Rohrer
                                                                                                                                           EST discovery in swine
-minmatch 12 options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled"
/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                346
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 119; DB 10;
Pred. No. 4.9e-23;
                                                                                                                                                                                      Grosse, W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                     NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                 cDNA
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d by cro
                                                                                                                                                                                                                                                                                                                       mRNA
9 5', m
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        led and alt_trimmed with phred
cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                               mRNA sequence
                                                                                                                                                                                                    ,G.A.,
                                                                                                                                                                                      Bennett, G.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
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                                                                                                                                                                                                    Smith, T
                                                                                                                                                                                                                               Euteleostomi;
Sus.
                                                                                                                                                                                                    .P.L.,
                                                                                                                                                                                       Laegreid, W.W.
                                                                                                                                                                                                                                                                                                                                                 EST 30-JUL-2001
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                                                                                                                                                                                                      Casas, E.
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                    18
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VERSION
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Matches
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                                                                                                                                                                                                                                                                                                                   AUTHORS
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                             source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CCAAAATTTGTGGCGCGCAGAAAATGTTGTTAATAACAGAAACCCAGCAAACATTCGTA 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tgctcacaatagttgc 346
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                                                                                                                                                                                                                   126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BE521841
M22AISTM Arabidopsis
clone M22Al 5', mRNA
                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                        Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Bo Zoology Bldg. 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
                                                                                                                    Tel: 517 355 1609
Fax: 517 353 9334
Email: benning@msu.edu
                                                                                                                                                                                             Dept. of Biochemistry & Molecular Biology Michigan State University
                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plate: 132 row: L column: 23
Seq primer: ATTTAGGTGACACTATAG.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR PRimers
FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                            thale cress.
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                                                                                                                                                                          Biochemistry, Michigan State University, East Lansing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: pCMV SPORT6; Site_1: xbaI; Site_2: xhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."

36 c 30 g 48 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9823"
/clone_11b="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/organism="Arabidopsis
/strain="Columbia"
                                          Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             29.0%;
92.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   336 bp developing sequence.
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Pred. No. 2.1e-20;
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               thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seed Arabidopsis thaliana cDNA
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                                                                      309 Botany & A, FAX:
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RESULT 10
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AUTHORS
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VERSION
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ORGANISM
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Best Local S
Matches 116
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ies 116; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Cathy Ronning
The Institute for Genomic Research
For clone info: please contact Research Genetics, Libraries
Division tel 1-800-711-6195, email cdna@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BI432815
178 bp mRNA line EST535576 P. infestans-challenged leaf Solanum PPCAWII 5' sequence, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Restrepo,S., Griffiths,H.M., Smart,C.D., Cho,J., Chiemingo,A., Bougri,O., Buell,C.R., Ronning,C.M., Fry,W.E. and Baker,B. Generation of ESTs from Potato Leaves Challenged with Phytopht
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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BI432815.1
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Restrepo, S., Griffiths, H.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Solanum tuberosum
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/note-"Vector: pBluescript SK(-); Site_1: EcoRI; Site_2: KhoI; Whole plants were challenged with 450,000 sporangia/ml P. infestans US-1(US 940501) in Biotron (Madison, Wisconsin). Leaf tissue was collected at 1, 2, 5, 12, and 24 hours post-challenge and frozen in liquid nitrogen immediately upon removal. Kennebec plants showed no signs of HR. Katahdin plants (susceptible to P. infestans US-1) were used as controls and showed infection. NOTE: We cannot exclude the possibility that this sequence is actually derived from Phytophthora rather than potato."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="M22A1"
/clone_llb="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="5-13 days after flowering"
/lab_host="5-101"
/note="0rgan: Developing seed; Vector: pBluescript SK-;
Site_1: EcoRI, Site_2: XhoII"
a 80 c 74 g 73 t
                                                                                                                                                                                                                             /clone_lib="P, infestan
/tissue_type="leaf"
/dev_stage="6 week old"
/lab_host="SOLR"
                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:4113"
/clone="ppCAW11"
                                                                                                                                                                                                                                                                                                                                                              /cultivar-"Kennebec"
                                                                                                                                                                                                                                                                                                                                                                             organism="Solanum tuberosum"
                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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Pred. No. 2.8e-20;
0; Mismatches 11
                                                                                                                                                                                                                                                                                           infestans-challenged leaf"
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                                                         33 catgcaggataataagatgaaaaaaatgttatttttctgccgctctggcaatgcttattac 92
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GCCAAAATTTGTGGCGGCG 79
                          gccaaaatttgtggcggtg 229
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                                                                                                                                                                                                                                                                                                                                                                                                 University of Washington Department of Molecular Biotechnology, Box 357730, University Washington, Seattle, WA 98195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prostate cancer expression profiling
Genomics 59 (2), 178-186 (1999)
99339982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 802)
Huang,G.M., Ng,W.l., Farkas,J., He,L., Llang,H.A.,
and Hood,L.
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Tel: 5106280100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Guyang Matthew Huang
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                                                                                                                     Conservative
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                                                                                                                                                                                                           /clone_11b="mynorm"
/clone_11b="mynorm"
/note="Organ: Prostate; Vector: pBluescript; Directional
/note="Organ: Prostate; Vector: pBluescript; Directional
/note="Organ: Prostate Isance constructed using Lambda ZP II kit
(Stratagene). mRNA was extracted from a frozen normal
(Stratagene). mRNA was extracted from a frozen normal
prostate tissue (Mayo Clinic)."
152 c 163 g 183 t 125 others
                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 1.1e-14;
0; Mismatches, 21;
                                                                                                                      Score 65.8; DB 9;
Pred. No. 6.2e-08;
0; Mismatches 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: oandersnepw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson, O.D., Butler, E., Chao, S., Choi, D.W., Close, T.J., Fenton, R.D., Gustafson, J.P., Han, P.S., Hsia, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Ross, K., Seaton, C.L. and Tong, J.C. The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BE493915.1 GI:9660508
AA547917 299 bp mRNA linear EST 22-SEP-1997 MB3D6V2G05T3 Brugia malayi day 6 post-infection third stage larvae SAW96MLW-BmL3d6 Brugia malayi cDNA clone 3D6V2G05 5', mRNA
                                                                                                                                                                                                                                                                                                                                         68
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Spermatophyta; Magnollophyta; Lillopsida;
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                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note-"Yector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: ECORI; Site_2: XhoI, Plants were grown in the
greenhouse. Anthers were harvested and pooled from early
meiosis to late meiosis. The tissue, total RNA, and
poly(A) RNA were prepared (Butler, Ross and Gustafson) at
University of Missouri, Columbia. A cDNA library was
made, and the CDNA clones were in vivo excised to give
pBluescript phagemids in the TJ Close lab (Choi, Close,
Fenton) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."

36 a 150 c 142 g 166 t
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/cultivar="Blanco"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="Adult plant before anthesis"
/lab_host="E_ coli SOLR"
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Pred. No. 3.2e-07
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a; Poales; Poaceae; Pooldeae
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                    ORGANISM
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                                                                                                                                                                                                                              AA547917
AA547917.1
                                                                                                                                                                                                                                                                                                    1 Similarity 89.: 49; Conservative
                                                                                                                       B84811
RPCI11-28F7.TP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: mark.blaxtereed.ac.uk
The ABI trace of this sequence can be viewed at
http://www.sanger.ac.uk/brugia/3D6/MB3D6V2G05T3.html
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genes expressed in day six post-infection, third stage larvae of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Blaxter, M.L., Waterfall, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
Onchocercidae; Brugia.
1 (bases 1 to 299)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brugia malayi.
Homo sapiens
Eukaryota; M
                                                                     B84811.1 GI:2925943
                                                                                                      sequence
                                      tuman .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 +44 131 650 6760
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                                                                                                                                                                                                                                                                                                                                                                                                   /note="vector: lambdaZapII (UniZap XR); Site_1: Eco R I
(5' end); Site_2: Xho I (3' end); Brugia malayi is a
lymphatic filarial nematode parasite of humans. mRNA was
prepared from third stage larvae of Brugia malayi isolated
from the peritoneal cavity of jirds six days after
infection. The mRNA was converted to double stranded cDNA
using reverse transcriptase and oligo(dT) followed by
RNase H and DNApol I. The library had 2 x 10E5 independent
recombinants and average insert size was 900 base pairs.
The library was constructed by Michelle Lizotte-Wanlewski.
The library is available from The Filarial Genome Project
Resource Center: contact Dr. S.A. Williams, Clark Science
Center, Smith College, Northampton, MA 01063 USA phone +1
413 885 3826 fax +1 413 585 3786 email genome@smith.edu."
89 a 81 c 70 g 59 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Brugia malayi"
/strain="TRS Labs"
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/lab_host="E. coli XL1-Blue"
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larvae SAW96MLW-BmL3d6"
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   Metazoa; Chordata;
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                                                                                                                       RPCI-11 Homo sapiens
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   Craniata; Vertebrata; Euteleostomi;
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c clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              269 ATTAGAACAAGACAAGGATGCTTACTTTTGCTACTCCCATCCAACATAGTACTAGAAGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 ataataagatgaaaaaatgttattttctgccgctctggcaatgcttattacaggatgtg 100
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GSS.
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                                                                                                                                                                          AQ309897 634
CITBI-E1-2522C23.TR CITBI-E1
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The Institute for Genomic Research
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Other_GSSs: RPCI11-28F7.TV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. Fo
Ilbrary availability, please contact Pleter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Use of BAC End Sequences for
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                                                                                                                                           DNA sequence.
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/note="Vector: pBACe3.6; Site_1:
/note="Vector: pBACe3.6; Site_1:
/note="Nector: pBACe3.6; Site_1:
/note="Lymphocytes"
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/db_xref="GDB:7510494"
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/clone="RPCI-11-28F7"
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Matches 122; Conserv
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549 TAGCATTTTT 558
                                                                      281 toggttttat 290
                                                                                                                                                  429 TATCTCTCATCATGGATTATAAAATTCTATACTAGAGAACCCTGGAGACACCACCAAAGA 488
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                                                                                                                                                                                                                                                                                                     309 ATTAGAACAAGACAAGGATGCTTACTTTTGCTACTCCCATCCAACATAGTACTAGAAGTG 368
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Seq primer: M13 Reverse
Class: BAC ends.
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Contact: Shaying Zhao, William Nierman, Mark. Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
712 Medical Center Dr., Rockville, MD 20850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Use of a random human BAC End Sequence Database for Sequence-Ready
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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301 838 0208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /cell_type="sperm"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"
123 c 89 g 148 t
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/db_xref="taxon:9606"
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Pred. No. 0.037;
0; Mismatches 128;
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Search completed: July 23, 2002, 13:10:30 Job time: 7536 sec

11-OCT-2001

WO200175067-A2 Homo sapiens.

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Query Match 10.:
Best Local Similarity 81.0
F. Matches 45; Conservative
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AAA26702
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                                                                                                                                                                                                                                                             diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutation responsible for genetic disorders or other traits and to assess
            Candida albicans infection; growth; survival; medicament; AIDS; vulvovaginitis; immunocompromised patient; treat; ss.
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P-PSDB; ABG29752.
                                                                Candida albicans polynucleotide sequence #40.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID No 29743; 103pp; English.
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                                                                                                     23-JUN-2000
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                                                                                                                                                                        AAA26702 standard; cDNA; 1685 BP
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23-AUG-2000; 2000US-0649167.
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                                                                                                     (first entry)
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81.8%;
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                                                                                                                 This sequence represents a polynucleotide sequence encoding a polypeptide that is critical for the survival and growth of Candida ablicans. The C. albicans nucleic acid molecules of the invention may be used as probes and primers for detecting homologous nucleic acid molecule sequences. The polypeptides and nucleic acid molecules and compounds identified as selectively modulating the expression of the polypeptides, may be used as medicaments or for the proparation of a medicament to treat Calbicans associated diseases, especially in AIDS patients and to treat Calbicans associated diseases, especially in AIDS patients and to treat Deputides and polynucleotide sequences to treat Calbicans associated diseases has fewer side effects and less toxicity than previously used methods such as the use of amphotericin. This method is therefore especially suitable for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Page 78; 133pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Essential polypeptides isolated from Candida albicans, treatment of diseases caused by C.albicans, especially immunocompromised subjects, e.g., AIDS patients -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-258614/23
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Sequence 1685 BP; 650 A; 281 C; 250 G; 504 T; 0 other;

Matches Query Match Local 62; Conservative 9.6%; 0; Score 36.2; DB Pred. No. 0.81; 0; Mismatches 43; 21; Indels Length 1685; 0; Gaps 0

밁 Ş 1334 142 acaccaaaggaaaccatcactcattcattcttcgtttcgggaattggacaagagaaaact 201 acaccaccggaaaccaccacttataattcatacgctagtgatatggaagaagatgaaatt 1393

δã 202 gttgatgcagccaaaatttgtggcggtgcagaaaatgttgttaaa 246

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Search completed: July 23, 2002, 13:51:26 Job time: 5377 sec

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Perfect score:
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1    /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

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4    /cgn2_6/ptodata/2/ina/6B_COMB.seq:*

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CITY: MI
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Sequence 189, Sequence 25,	92,	5	•	84,	Sequence 84,		Sequence 84,	Sequence 1,	Sequence 15,		Sequence 15,		Sequence 11,	Sequence 11,	Sequence 1,	Sequence 1,
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## ALIGNMENTS

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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (gen
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APPLICANT: NOLAN, LISA K.

APPLICANT: HORNE, SHELLEY M.

TITLE OF INVENTION: DNA ENCODING AI

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

CORRESPONDENCE MUETING, RAASCH & GEB
                                                                                                                                                   TELEPHONE: (612) 305-
TELEFAX: (612) 305-12:
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010101
                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
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5. 6087128
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Query Match 100.0%; Score 378; DB 4; Length 378; Best Local Similarity 100.0%; Pred. No. 3.2e-112;
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STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: I
US-09-282-352A-21
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US-09-282-352A-21
                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARR: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999
CLASSIFICATION DATA:
APPLICATION NUMBER: US 09/023,221
PILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 255.00010102
FELEPONE: (612) 305-1226
FELEPAX: (612) 305-1226
FELEPAX: (612) 305-1226
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 base pairs
FTPE: nucleic acid
STRANDENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21, Application US/09282352A Patent No. 6187321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT: NOLAN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        301 ATCTATACTCCGCTGGAAGCCCGGGTATATTGCTCACAATAGTTGCCCCATCGATATGGGG 360
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: MINNEAPOLIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 55401
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                 DNA (genomic)
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RESULT 3 US-09-023-22: Sequence 1 Patent No. GENERAL II APPLICAL CORRESPO ADDRES STATE COMPUTE E COMPUTE APPLICAL APPLIC	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	Matches Qy 1
Unence 1, in month of the control of	61 61 221 221 221 441 661 661 661 661	
T 3 -023-221A-1 uence 1, App ent No. 6087 NERAL INFOM NERAL INFOM APPLICANT: APPLICANT: APPLICANT: APPLICANT: YITLE OF INV COUNTRY: INV COUNTRY: LIP: 5540 COMPUTER RESPINATE: MIN STATE: MIN STATING PELLETAN: APPLICATIO APPLICANT APPLICATIO APPLICATIO APPLICATIO APPLICATIO APPLICATIO APPLICANT APPLICATIO APPLICATIO APPLICATIO APPLICANT APPL	TIGGA TITATI TATI TATI GGAAA GGAAA TITAA TITAA TITAA TITAA TITAA TITAA TITAA TITAA	378; tgga
ULT 3 09-033-221A-1 09-033-221A-1 09-033-221A-1 09-033-221A-1 09-033-221A-1 atent NO. 6087128 GENERAL INFORMATION APPLICANT: HORNE, TITLE OF INVENTION UNDBER OF SEQUENCY CORRESPONDENCE AUE STREET: 119 NOI CORPETER MINNEAPOL STATE: MN COUNTRY: U.S.A ZIP: 55401 COMPUTER READABLE MEDIUM TYPE: PATE OPERATING SYSTE SOFTWARE: PATE CURRENT APPLICATION APPLICATION NUM APPLICATION NUM FILING DATE: 11 CLASSIFICATION NUM REFERENCE/DOCKES ATTORNEY/AGENT INI NAME: SAUDBERG REGISTRATION NUM REFERENCE/DOCKES SEQUENCE CHARACTER ATTORNEY/AGENT INI NAME: SAUDBERG REGISTRATION FOR SEQ SEQUENCE CHARACTER LENGTH: 760 bas TIPE: nucleic a STOPOLOGY: 1 ince TOPOLOGY:	AGTT IIII IIIII ICAAA ICAAAA ICAAAA ICAAAA ICAAAA ICAAAA ICAAAA	raget Co
USERGISTRATION UNMERRE CURRENT APPLICATION US APPLICANT: HORNE, SHEL TITLE OF INVENTION: DN UNDER OF SEQUENCES: ADDRESSEE: MUETING, STREET: 119 NORTH FO CITY: MINNEAPOLIS STATE: MN COUNTRY: U.S.A. ZIP: 55401 Z	CTGGAAGTTCTGTTCCAG  ttattttctgccgctctg	nserv ctgtt
	TTCAG TTCAG	Conservative ttctgttccagg
US/0902322  US/0902322  ISA K.  BISA ENCODI  2 2 2 2 3 2 3 2 5 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	GGGCC 	999cc
/09023221A  K. LEY M. LEY M. A ENCODING A PACTORIA & GEE URTH STREET, DOS,MS-DOS elease #1.0, Elease #1.0, UCTORIA A. VICTORIA	CCTG GCTH ACCA TGATH TGATH FIGHT 199ta	0; 
IG AN AVI. GEBHARDTET, SUIT OO0010101	GGATC	Misma ggato
9023221A  ENCODING AN AVIAN  ASCH & GEBHARDT P.  TH STREET, SUITE 2  TH STREET, SUITE 2  SAMS-DOS ease #1.0, Version 98 ease #1.0, Version 1: 255.00010101  TION: 226 1: 1:	CTGGAAGTTCTAGGGGCCCCTGGGATCAGGATAAGAATAGATGAAAAAATGCTTCTAGGCGCCCCTGGGATCAGGATAAGAATGCTTAATAAAAATGCTTTTCTGCCGCTCTGGCAATGCTTATTACAGGATGTGCCCAACAAAAATGCTTTACTTTCTGCCGCTCTGGCAATGCTTATTACAGGATGTGCCCAACAAAAAGGTTAACTGTTTTCTGCCGCTCTGGCAATGCTTATTACAGGATGTGCCCAACAAAAAGGTTAACTGTTTGTGGCGAACAACAACGTTTACTGTTTGGTGGAAAAAAAA	378; Conservative 0; Mismatches 0; Indels 0; Gi ctggaagttctgttccaggggcccctgggatccatgcaggataataagatgaaaaaaatg
о 203 #1	AGGA [1]	agga 
COLI	TAATI	O;
ISS	AGATAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAGATAAAAAGATAAAAAA	Indels aagatg
	GAAAA grtts GTTTI CTTCC CTTCC HILL CAAAA AGAAA AGAAA AGAAA AGAAA AGAAA AGAAA AGAAA AGAAA AGAAA	gaaas
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US-09-282-352A-1
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US-09-282-352A-1
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                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release $1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 55401
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: ROBINSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI
TUDBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                  NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERRICE/DOCKET NUMBER: 255.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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               MOLECULE TYPE:
                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
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STATE: MN
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                            TOPOLOGY: linear
                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/09/282,352A FILING DATE: 31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                         LENGTH:
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                                                   : 760 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HORNE, SHELLEY M.
                                                                                                                         (612) 305-1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                 U.S.A.
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           DNA (genomic)
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                                                                                                                                                                      255.00010102
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                                                                                                                                                                                                                                                                                                                                                  Version
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RESULT 5
US-09-023-221A-22
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                             TELEFAX: (612) 305-1228 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 309 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,221A
FILING DATE: 12-FEB-1998
CINCLESTED ATTENTION AT
                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: NOLAN, LISA K. APPLICANT: HORNE, SHELLEY M.
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                579
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                                                                                             TYPE: nucleic acid
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ZIP: 55401
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
                                                                STRANDEDNESS:
                                       TOPOLOGY:
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    Application US/09023221A
6087128

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DNA (genomic)
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Pred. No. 8.1e-100;
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EET, SUITE 203
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       quence 22, Application US/09282352A
tent No. 6187321
                                                                                                     TELEFAX: (612) 305-12: NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 09/023,221
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: SANDBERG MS., VICTORIA A.
REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00010102
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READNALE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATENG PROFESSION PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: NOLAN, LISA K.
APPLICANT: HORNE, SHELLEY M.
APPLICANT: ROBÎNSON, MICHAEL
TITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI ISS
NUMBER OF SEQUENCES: 22
                                               SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
TYPE: pucleic acid
                                                                                                                                    TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                STRANDEDNESS:
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TOPOLOGY: 1
LECULE TYPE:
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31-MAR-1999
DNA (genomic)
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; MOLECULE TYPE:
JS-09-023-221A-5
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Best Local Sin
Matches 309;
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                                                                                                       TELEFAX: (612) 305-1228 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                             TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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APPLICANT: HORNE,
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                       NAME: SANDBERG MS., VICTORIA A. REGISTRATION NUMBER: 41,287
                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/023,221A FILING DATE: 12-FEB-1998
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                                                        STRANDEDNESS:
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                                                                                        LENGTH:
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                                     "OPOLOGY: linear
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HORNE, SHELLEY M.
VENTION: DNA ENCODING AN AVIAN
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Pred. No. 4.2e-90;
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Best Local Similarity
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                                                                                      TELEFAX: (612) 305-12
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 309 base pairs
                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                            APPLICATION NUMBER: US 0 FILING DATE: 12-FEB-1998 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
MOLECULE TYPE:
                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (612) 305-1226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
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                                                                                                                                              NAME: SANDBERG MS., VICTORIA A. REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00
                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: MINNEAPOLIS
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                                                                                                                                                                                                                                                          FILING DATE: 3
CLASSIFICATION:
                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/OFFILING DATE: 31-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
               TOPOLOGY:
                           STRANDEDNESS:
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                                                                                                                   TELEPHONE:
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VENTION: DNA ENCODING AN AVIAN E. COLI ISS
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153 aaccatcactcattcattcttcgtttcgggaattggacaagagaaaactgttgatgcagc 212

9294 catcgggaataacaccatgaaaaaaatgctactcgctactgcgctggccctgcttattac 9353

93 aggatgtgctcaacaacgtttactgttggaaacaaaccgacagcagtaacaccaaagga 152

aggatgtgctcaacagacgtttactgttcaaaaccaaaccggcagcagtagcaccaaagga 9413

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SEQ ID NO 13
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Best Local
                                                                  Query Match
Best Local Similarity
                                                   Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Patent No.
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 15
                                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
                                                                                                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 09/364,862
EARLIER FILING DATE: 1999-07-30
                                                                                                                                                                                                                                                                                          EARLIER FILING DATE: 1998-10-20
                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 60/125,974
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Couto, Linda B.
APPLICANT: Colosi, Peter C
                                                                                                                                                                                    TYPE: DNA ORGANISM: Artificial Sequence
                                                                                                                                                                      FEATURE:
                                                                                                                                                                                                                    LENGTH: 11933
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33 catgcaggataataagatgaaaaaaatgttattttctgccgctctggcaatgcttattac 92
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88.5%;
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                                                                Score 256.4; DB 4
Pred. No. 1.7e-72;
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Pred. No. 1.
                                                   Mismatches
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US-09-364-862-13
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Best Local Similarity 88.9
Matches 278; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/364,862
CURRENT FILING DATE: 1999-07-30
EARLIER APPLICATION NUMBER: 60/125,974
EARLIER FILING DATE: 1999-03-24
EARLIER APPLICATION NUMBER: 60/104,994
EARLIER FILING DATE: 1998-10-20
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Couto, Linda B.
APPLICANT: Colosi, Peter C.
TITLE OF INVENTION: ADENO-ASSOCIATED VECTORS FOR EXPRESSION OF FACTOR VIII
TITLE OF INVENTION: BY TARGET
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
TITLE OF INVENTION: CELLS
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                            aaccatcactcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagc
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                                                                                                                                                                            casaatttgtggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaa
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                                                                                                                                                                                                                                                                                                                                                         catcgggaataacaccatgaaaaaatgctactcgctactgcgctggccctgcttattac 9353
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Pred. No. 1.7e-72;
0; Mismatches 36;
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US-09-282-352A-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: SANDBERG MS. VICTORIA A. REGISTRATION NUMBER: 41,287
REFERENCE/DOCKET NUMBER: 255.00
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
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ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
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                                                                                                                               GGATTGCTCGGTTTTATTACTTTAGGCATTTATACTCCGCTGGAAGCGCGTGTGTATTGC
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SHELLEY M.
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88.6%;
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Length 309 Indels

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Best Local Similarity
Matches 273; Conserv
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NFORMATION FOR SEQ ID NO:
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APPLICATION NUMBER: US/09/282,352A
FILING DATE: 31-MAR-1999
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
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ADDRESSEE: MUETING, RAASCH & GEBHARDT P.A.
STREET: 119 NORTH FOURTH STREET, SUITE 203
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NAME: SANDERG MS., VICTORIA A.
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REFERENCE/DOCKET NUMBER: 25
FELECOMMUNICATION INFORMATION:
TELEPHONE: (612) 305-1226
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FITLE OF INVENTION: DNA ENCODING AN AVIAN E. COLI
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TCACAATA 308
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                                                                   GGATTGCTCGGTTTTATTACTTTAGGCATTTATACTCCGCTGGAAGCGCGTGTGTATTGC
                                                                                 ggattgctcggttttatcacttttggcatctatactccgctggaagcccgggtatattgc 333
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Pred. No. 8.4e-72;
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Patent No.
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Best Local S
Matches 48
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                                                                                    GENERAL INFORMATION:
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                         APPLICANT:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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NAME: Bloom, Allen
REGISTRATION NUMBER: 29,
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                                                                      APPLICANT:
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APPLICATION NUMBER:
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OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
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    Application US/08743637B
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                                      BERGERON, Michel G.
PICARD, Francois J.
OUELLETTE, Marc
                         ROY, Paul
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SPECIES-SPECIFIC AND UNIVERSAL DNA
PROBES AND AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND
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Building
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                                                                                                                                                                                                                                                                                                        Score 34.2; DB Pred. No. 0.15; Mismatches
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                                                                                                                                                                                                                                                                                                                                    DB 4;
                                                                                                                                                                                                                                                                                                          23;
                                                                                                                                                                                                                                                                                                                                    Length 1519;
                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                          Gaps
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CORRESPONDENCE ADDRESS: TITLE OF INVENTION: NUMBER OF SEQUENCES:

CITY: MILWAUKEE

STREET: ADDRESSEE:

411 EAST WISCONSIN AVENUE

QUARLES & BRADY

IDENTIFY COMMON BACTERIAL PATHOGENS AND ASSOCIATED ANTIBIOTIC RESISTANCE GENES FROM CLINICAL SPECIMENS

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                              APPLICANT: OUELLETTE, MAIC APPLICANT: ROY, Paul H. TITLE OF INVENTION: SPECIFIC TITLE OF INVENTION:
                                                                                                                                                                    equence 1, Application US/08526840B atent No. 6001564
                                                                                                                                                       ENERAL INFORMATION:
                                                                                                                                                                                                                                                                 1211 ACGTATGCTTCCTCTTTAGATGTAGTTGGTCATGAAATGACACATGGTGTGACGGAACAT 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 35,433
REGISTRATION NUMBER: 35,433
REFERENCE/DOCKET NUMBER: 85TELECOMMUNICATION INFORMATION:
TELEPHONE: /414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: (FILING DATE: 04-NOV-1
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  220 tgtggcggtgcagaaatgttgttaaaacagaaactcagcaaacattcgtaaatggattg 279
                                                                                                                                                                                                                                                                                                                                                                                                             160 actcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagccaaaatt 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPAtible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US 08/526,840 FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WISCONSIN
                                                                                                                                     BERGERON, Michel G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
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QUARLES & BRADY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9%;
                            SPECIFIC AND UNIVERSAL PROBES AND
AMPLIFICATION PRIMERS TO RAPIDLY DETECT AND IDENTIFY
COMMON BACTERIAL PATHOGENS AND ANTIBIOTIC RESISTANCE GENES
FROM CLINICAL SPECIMENS FOR ROUTINE DIAGNOSIS IN ...
177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33.6; DB Pred. No. 0.25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 1817;
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Search completed: July 23, 2002, 13:45:07 Job time: 5108 sec

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                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                Query Match 8.9%;
Best Local Similarity 51.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (414) 277-5591
INFORMATION FOR SEQ ID NO: 1:
1331 ATGGGTTATATTATTTCGGGTGCATCTAATCC
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1817 base pair
                                                               1211 ACGTATGCTTCCTCTTTAGATGTAGTTGGTCATGAAATGACACATGGTGTGACGGAACAT 1270
                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 850586.90012 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 12-SEP-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                             160 actcatcatttcttcgtttcgggaattggacaagagaaaactgttgatgcagccaaaatt 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                            220 tgtggcggtgcagaaaatgttgttaaaacagaaactcagcaaacattcgtaaatggattg 279
                               280 ctcggttttatcacttttggcatctatactcc 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 411 East CITY: Milwaukee
                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 53202-4497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/526,840B FILING DATE: 11-SEP-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                  78;
                                                                                                                                                                                                                                                                                                                                                                                   : 1817 base pairs
nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BAKER, Jean C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wisconsin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             411 East Wisconsin Avenue
                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                     linear
                                                                                                                                                                                                                                                                                                   Enterococcus faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (414)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Floppy dish
                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                   double
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                                                                                                                                                                                                                Score 33.6; DB Pred. No. 0.25;
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1362
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                                                                                                                                                                                                Indels
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